

## Appendix IV

### Alignment of instant SEQ ID NO: 3 with GenBank Accession No. K00470

>gb|K00470.1|HUMAN Homo sapiens growth hormone variant precursor (GH-V) gene, complete cds  
Length=2660

GENE ID: 2689 GH2 | growth hormone 2 [Homo sapiens] (Over 18 PubMed links)

Score = 4913 bits (2660), Expect = 0.0  
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)  
Strand=Plus/Plus

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Query    1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT 60
          |||
Sbjct    1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT 60

Query    61      TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCCGGGAGGAGGAAAG 120
          |||
Sbjct    61      TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCCGGGAGGAGGAAAG 120

Query    121     GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180
          |||
Sbjct    121     GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180

Query    181     TCCTTCTCCGCGTTCAGGTTGGGCCACCATGGGCTGCTGCCAGAGGGGCACCCACGTGACCC 240
          |||
Sbjct    181     TCCTTCTCCGCGTTCAGGTTGGGCCACCATGGGCTGCTGCCAGAGGGGCACCCACGTGACCC 240

Query    241     TTAAAGAGAGGACAAAGTTGGGTGGTATCTCTGGCTGACATCTGTGCACAAACCTCACAA 300
          |||
Sbjct    241     TTAAAGAGAGGACAAAGTTGGGTGGTATCTCTGGCTGACATCTGTGCACAAACCTCACAA 300

Query    301     CGCTGGTGTATGGTGGGAAGGGAAGATGACAAAGTCAGGGGGCATGATCCCAGCATGTGTG 360
          |||
Sbjct    301     CGCTGGTGTATGGTGGGAAGGGAAGATGACAAAGTCAGGGGGCATGATCCCAGCATGTGTG 360

Query    361     GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCATAACATG 420
          |||
Sbjct    361     GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCATAACATG 420

Query    421     CAGAGAAACAGGTGAGGAGAAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCAC 480
          |||
Sbjct    421     CAGAGAAACAGGTGAGGAGAAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCAC 480

Query    481     AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC 540
          |||
Sbjct    481     AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC 540

Query    541     AGCTCACTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTTGGCACAATGTGT 600
          |||
Sbjct    541     AGCTCACTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTTGGCACAATGTGT 600

Query    601     CCTGAGGGGAGAGGCGCGCTCTGTAGATGGGACGGGGGCACATAACCCCTCAGGTTTGGGG 660
          |||
Sbjct    601     CCTGAGGGGAGAGGCGCGCTCTGTAGATGGGACGGGGGCACATAACCCCTCAGGTTTGGGG 660

Query    661     CTTATGAATGTTAGCTATCGCCATCTAAGCCCAAGTATTTGGCCAAATCTCTGAATGTTTCT 720
          |||
Sbjct    661     CTTATGAATGTTAGCTATCGCCATCTAAGCCCAAGTATTTGGCCAAATCTCTGAATGTTTCT 720

Query    721     GGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
          |||
Sbjct    721     GGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

Query    781     GAGAGCGCTGGCCCTCTTGTCTCTCCAGCTCCCTCTGTTGCCCTCCGGTTTCTCCCAAGGCTC 840
          |||
Sbjct    781     GAGAGCGCTGGCCCTCTTGTCTCTCCAGCTCCCTCTGTTGCCCTCCGGTTTCTCCCAAGGCTC 840

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Query	841	CCGGACGTCCTGCTCCTGGCTTTTGGGCTGCTCTGCTGCTGCTGCTGCTTCAAGAGGGCAG	900
Sbjct	841	CCGGACGTCCTGCTCCTGGCTTTTGGGCTGCTCTGCTGCTGCTGCTTCAAGAGGGCAG	900
Query	901	TGCGCTTCCCAACCATTCCTTATCCAGGCTTTTGGACAACGCTATGCTCCCGGCCCGCTCG	960
Sbjct	901	TGCGCTTCCCAACCATTCCTTATCCAGGCTTTTGGACAACGCTATGCTCCCGGCCCGCTCG	960
Query	961	CCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGGGTGC	1020
Sbjct	961	CCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGGGTGC	1020
Query	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCGCGCTGGGAAGTAATGGGAGGAGACTA	1080
Sbjct	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCGCGCTGGGAAGTAATGGGAGGAGACTA	1080
Query	1081	AGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGTGAG	1140
Sbjct	1081	AGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGTGAG	1140
Query	1141	GTTCCAGAAAAGTAACAATGGGAGCAGGCTCTCCAGCATAGACCTTGGTGGGCGGTCTCT	1200
Sbjct	1141	GTTCCAGAAAAGTAACAATGGGAGCAGGCTCTCCAGCATAGACCTTGGTGGGCGGTCTCT	1200
Query	1201	CTCCTAGGAAGAAGCCTATATCTCTGAAGGAGCAGAAGTATTCTCTGCAAGACCCCCA	1260
Sbjct	1201	CTCCTAGGAAGAAGCCTATATCTCTGAAGGAGCAGAAGTATTCTCTGCAAGACCCCCA	1260
Query	1261	GACCTCCCTCTGCTTCTCTCAGAGTCTATTCCAAACACCTTCCAACAGGGTGAAAACGCAGCA	1320
Sbjct	1261	GACCTCCCTCTGCTTCTCTCAGAGTCTATTCCAAACACCTTCCAACAGGGTGAAAACGCAGCA	1320
Query	1321	GAAATCTGTGAGTGGATGCGCTTCTCCCCAGGTGGGATGGGGTAGACCTGTGGTCAAGGCC	1380
Sbjct	1321	GAAATCTGTGAGTGGATGCGCTTCTCCCCAGGTGGGATGGGGTAGACCTGTGGTCAAGGCC	1380
Query	1381	CCCGGGCAGCACAGCCACTGCGCGCTCTTCCCTGCGAGAACCCTAGAGCTGCTCCGCATCT	1440
Sbjct	1381	CCCGGGCAGCACAGCCACTGCGCGCTCTTCCCTGCGAGAACCCTAGAGCTGCTCCGCATCT	1440
Query	1441	CCCTGCTGCTCATCCAGTCAATGCTGGAGCCCGCTGCAGCTCCTCAGGAGCGTCTTCGCCA	1500
Sbjct	1441	CCCTGCTGCTCATCCAGTCAATGCTGGAGCCCGCTGCAGCTCCTCAGGAGCGTCTTCGCCA	1500
Query	1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCTAGAGG	1560
Sbjct	1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCTAGAGG	1560
Query	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCCAATCTTGGGGCCCCAC	1620
Sbjct	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCCAATCTTGGGGCCCCAC	1620
Query	1621	TGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCGCTCTTTTTAGCAGTCAGGCGCTGA	1680
Sbjct	1621	TGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCGCTCTTTTTAGCAGTCAGGCGCTGA	1680
Query	1681	CCCAAGAGAACTCACCCTATCTCTCATTTCCCTCTGTAATCTCCAGGCGCTTTCTCTAC	1740
Sbjct	1681	CCCAAGAGAACTCACCCTATCTCTCATTTCCCTCTGTAATCTCCAGGCGCTTTCTCTAC	1740
Query	1741	AACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCG	1800
Sbjct	1741	AACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCG	1800
Query	1801	CTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACT	1860
Sbjct	1801	CTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACT	1860
Query	1861	GGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACGATGACGCA	1920
Sbjct	1861	GGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACGATGACGCA	1920
Query	1921	CTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCTGAGACA	1980
Sbjct	1921	CTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCTGAGACA	1980
Query	1981	TTCCTGCGCATCTGTCAGTGCCTCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGG	2040
Sbjct	1981	TTCCTGCGCATCTGTCAGTGCCTCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGG	2040

Query	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTG	2100
Subject	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTG	2100
Query	2101	CCCACCAGCCTTGTCTAATAAAATTAAAGTTGCATCATTTTGTTTGACTAGGTGTCCCTTG	2160
Subject	2101	CCCACCAGCCTTGTCTAATAAAATTAAAGTTGCATCATTTTGTTTGACTAGGTGTCCCTTG	2160
Query	2161	TATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAAC	2220
Subject	2161	TATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAAC	2220
Query	2221	CTGTAGGGCCTTCAGGGTCTATTTCGGGAACCAAGGCTGGAGTGCAGTGGCAGTCTTGGCTC	2280
Subject	2221	CTGTAGGGCCTTCAGGGTCTATTTCGGGAACCAAGGCTGGAGTGCAGTGGCAGTCTTGGCTC	2280
Query	2281	GCTGCAATCTCCGCCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCGAATAGTTG	2340
Subject	2281	GCTGCAATCTCCGCCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCGAATAGTTG	2340
Query	2341	CGATTCCAGGCATGCAAGACCAGGCTCAGCTAAATTTTGTATTTTGGTAGAGACGGGGT	2400
Subject	2341	CGATTCCAGGCATGCAAGACCAGGCTCAGCTAAATTTTGTATTTTGGTAGAGACGGGGT	2400
Query	2401	TTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCGCCTCGG	2460
Subject	2401	TTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCGCCTCGG	2460
Query	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATTT	2520
Subject	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATTT	2520
Query	2521	TAAAAATAATTATACCAGCAGAAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCCC	2580
Subject	2521	TAAAAATAATTATACCAGCAGAAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCCC	2580
Query	2581	AGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCTCTCATGCATTGGGTCCACTC	2640
Subject	2581	AGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCTCTCATGCATTGGGTCCACTC	2640
Query	2641	AGTAGATGCTTGTGAATTC	2660
Subject	2641	AGTAGATGCTTGTGAATTC	2660